SEQUENCE LISTING

<110> Merck & Co., Inc.
     Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.

<120> HCV REPLICONS CONTAINING NS5B FROM
  GENOTYPE 2B

<130> 21564Y PCT

<150> 60/517,605
<151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> modified NS5B

<221> VARIANT
<222> (5)...(5)
<223> Xaa = threonine or serine

<221> VARIANT
<222> (24)...(24)
<223> Xaa = asparagine or serine

<221> VARIANT
<222> (31)...(31)
<223> Xaa = methionine or isoleucine

<221> VARIANT
<222> (376)...(376)
<223> Xaa = isoleucine or leucine

<400> 1
Ser Met Ser Tyr Xaa Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly Pro
 1   5   10   15
Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg
                20   25   30
Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg
            35   40   45
Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His Tyr
        50   55   60
Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser Ala
65   70   75   80
Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His Ser
                85   90   95

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Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu Ser
        100                     105                     110
Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu Glu
        115                     120                     125
Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
    130                     135                     140
Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu Ile
145                     150                     155                 160
Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
                165                     170                     175
Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr Gly
                180                     185                     190
Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala Trp
        195                     200                     205
Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
    210                     215                     220
Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr
225                     230                     235                 240
Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu
                245                     250                     255
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln
                260                     265                     270
Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser
        275                     280                     285
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys
    290                     295                     300
Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu
305                     310                     315                 320
Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu
                325                     330                     335
Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
                340                     345                     350
Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
        355                     360                     365
Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Arg Tyr Phe Leu
    370                     375                     380
Thr Arg Asp Pro Thr Thr Pro Xaa Thr Arg Ala Ala Trp Glu Thr Val
385                     390                     395                 400
Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala
                405                     410                     415
Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser Ile
            420                     425                     430
Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr
        435                     440                     445
Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu
    450                     455                     460
Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His
465                     470                     475                 480
Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro
                485                     490                     495
Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile
            500                     505                     510
Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp
        515                     520                     525
```

```
Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser Arg
    530                 535                 540
Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp Ile
545                 550                 555                 560
Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu Leu Cys Leu
                565                 570                 575
Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu Pro Asp Arg
            580                 585                 590
```

<210> 2
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> modified NS5B

<221> variation
<222> (3)...(3)
<223> n = A or T

<221> variation
<222> (9)...(9)
<223> n = C or A

<221> variation
<222> (13)...(13)
<223> n = A or T

<221> variation
<222> (15)...(15)
<223> n = A or C

<221> variation
<222> (21)...(21)
<223> n - A or G

<221> variation
<222> (24)...(24)
<223> n = C or G

<221> variation
<222> (28)...(28)
<223> n = T or C

<221> modified_base
<222> (30)...(30)
<223> n = G or C

<221> variation
<222> (33)...(33)
<223> n = C or A

<221> variation
<222> (71)...(71)

<223> n = A or G

<221> variation
<222> (83)...(83)
<223> n = G or T

<221> variation
<222> (1174)...(1174)
<223> n = A or C

<400> 2

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acctcgagga gtgcctctct gagggcaaag aaggtgactt ttgacagggt gcaggtgctg  180
gacgcacact atgactcagt cttgcaggac gttaagcggg ccgcctctaa ggttagtgcg  240
aggctcctca cggtagagga agcctgcgcg ctgaccccgc cccactccgc caaatcgcga  300
tacggatttg gggcaaaaga ggtgcgcagc ttatctagga gggccgttaa ccacatccgg  360
tccgtgtggg aggacctcct ggaagaccaa cataccccaa ttgacacaac tatcatggct  420
aaaaatgagg tgttctgcat tgatccaact aaaggtggga aaaagccagc tcgcctcatc  480
gtataccccg accttggggt cagggtgtgc gaaaagatgg ccctctatga catcgcacaa  540
aagcttccca aagcgataat ggggccatcc tatgggttcc aatactctcc cgcagaacgg  600
gtcgatttcc tcctcaaagc ttggggaagt aagaaggacc caatgggggtt ctcgtatgac  660
acccgctgct ttgactcaac cgtcacggag agggacataa gaacagaaga atccatatat  720
caggcttgtt ctctgcctca agaagccaga actgtcatac actcgctcac tgagagactt  780
tacgtaggag ggcccatgac aaacagcaaa gggcaatcct gcggctacag gcgttgccgc  840
gcaagcggtg ttttcaccac cagcatgggg aataccatga catgttacat caaagccctt  900
gcagcgtgta aggctgcagg gatcgtggac cctgttatgt tggtgtgtgg agacgacctg  960
gtcgtcatct cagagagcca aggtaacgag gaggacgagc gaaacctgag agctttcacg 1020
gaggctatga ccaggtattc cgcccctccc ggtgaccttc ccagaccgga atatgacttg 1080
gagcttataa catcctgctc ctcaaacgta tcggtagcgc tggactctcg gggtcgccgc 1140
cggtacttcc taaccagaga ccctaccact ccantcaccc gagctgcttg ggaaacagta 1200
agacactccc ctgtcaattc ttggctgggc aacatcatcc agtacgcccc cacaatctgg 1260
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caaaatctca attttgagat gtacggggca gtatactcgg tcaatccatt agacctaccg 1380
gccataattg aaaggctaca tgggcttgaa gccttttcac tgcacacata ctctccccac 1440
gaactctcac gggtggcagc aactctcaga aaacttggag cgcctcccct tagagcgtgg 1500
aagagtcggg cgcgtgccgt gagagcttca ctcatcgccc aaggagcgag ggcggccatt 1560
tgtggccgct acctcttcaa ctgggcggtg aaaacaaagc tcaaactcac tccattgccc 1620
gaggcgagcc gcctggattt atccgggtgg ttcaccgtgg gcgccggcgg gggcgacatt 1680
tatcacagcg tgtcgcatgc ccgacccgc ctattactcc tttgcctact cctacttagc 1740
gtaggagtag gcatctttt actccccgat cgatga                             1776
```

<210> 3
<211> 1394
<212> PRT
<213> Artificial Sequence

<220>
<223> modified NS3-5A

<221> VARIANT
<222> (1215)...(1215)
<223> Xaa = asparagine or serine

<221> VARIANT

<222> (904)...(904)
<223> Xaa = valine or alanine

<400> 3
```
Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
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Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
            20                  25                  30
Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
        35                  40                  45
Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
    50                  55                  60
Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
65                  70                  75                  80
Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr
                85                  90                  95
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
            100                 105                 110
Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
            115                 120                 125
Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
    130                 135                 140
Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
145                 150                 155                 160
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met
                165                 170                 175
Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
            180                 185                 190
Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
        195                 200                 205
Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
    210                 215                 220
Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
225                 230                 235                 240
Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
                245                 250                 255
Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly
            260                 265                 270
Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
            275                 280                 285
Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile
    290                 295                 300
Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
305                 310                 315                 320
Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
                325                 330                 335
Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
            340                 345                 350
Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe
            355                 360                 365
Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
    370                 375                 380
Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
385                 390                 395                 400
```

```
Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met
                    405                   410                   415
Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
                420                   425                   430
Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
            435                   440                   445
Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly
    450                   455                   460
Arg Thr Gly Arg Gly Arg Met Gly Ile Tyr Arg Phe Val Thr Pro Gly
465                   470                   475                   480
Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr
                485                   490                   495
Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val
                500                   505                   510
Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
        515                   520                   525
His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp
    530                   535                   540
Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr
545                   550                   555                   560
Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
                565                   570                   575
Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr
                580                   585                   590
Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
                595                   600                   605
Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met
    610                   615                   620
Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly
625                   630                   635                   640
Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val
                645                   650                   655
Ile Val Gly Arg Ile Ile Leu Ser Gly Arg Pro Ala Ile Val Pro Asp
                660                   665                   670
Arg Glu Phe Leu Tyr Gln Glu Phe Asp Glu Met Glu Glu Cys Ala Ser
        675                   680                   685
His Leu Pro Tyr Ile Glu Gln Gly Met Gln Leu Ala Glu Gln Phe Lys
    690                   695                   700
Gln Lys Ala Leu Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala
705                   710                   715                   720
Ala Ala Pro Val Val Glu Ser Lys Trp Arg Ala Leu Glu Thr Phe Trp
                725                   730                   735
Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly
        740                   745                   750
Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe
    755                   760                   765
Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln Ser Thr Leu Leu Phe
    770                   775                   780
Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala
785                   790                   795                   800
Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Val Gly Ser
                805                   810                   815
Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
                820                   825                   830
```

```
Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Met
        835             840             845
Pro Ser Thr Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
    850             855             860
Gly Ala Leu Val Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His
865             870             875             880
Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
            885             890             895
Phe Ala Ser Arg Gly Asn His Xaa Ser Pro Thr His Tyr Val Pro Glu
        900             905             910
Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
        915             920             925
Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser
    930             935             940
Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys
945             950             955             960
Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro
            965             970             975
Gln Leu Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly
            980             985             990
Val Trp Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala
        995             1000            1005
Gln Ile Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro
    1010            1015            1020
Lys Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr
1025            1030            1035            1040
Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala
            1045            1050            1055
Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly
            1060            1065            1070
Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro
        1075            1080            1085
Cys Gln Val Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg
    1090            1095            1100
Leu His Arg Tyr Ala Pro Ala Cys Arg Pro Leu Leu Arg Glu Glu Val
1105            1110            1115            1120
Thr Phe Gln Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro
            1125            1130            1135
Cys Glu Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp
        1140            1145            1150
Pro Ser His Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly
        1155            1160            1165
Ser Pro Pro Ser Leu Ala Ser Ser Ser Ala Ile Gln Leu Ser Ala Pro
    1170            1175            1180
Ser Leu Lys Ala Thr Cys Thr Thr His His Val Ser Pro Asp Ala Asp
1185            1190            1195            1200
Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Xaa Ile
            1205            1210            1215
Thr Arg Val Glu Ser Glu Asn Lys Val Val Val Leu Asp Ser Phe Asp
            1220            1225            1230
Pro Leu Arg Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu
        1235            1240            1245
Ile Leu Arg Lys Ser Lys Lys Phe Pro Ala Ala Met Pro Ile Trp Ala
    1250            1255            1260
```

```
Arg Pro Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp
1265             1270             1275             1280
Tyr Val Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ile Lys Ala
            1285             1290             1295
Pro Pro Ile Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Thr Glu
            1300             1305             1310
Ser Ser Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly
        1315             1320             1325
Ser Ser Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Leu Pro
    1330             1335             1340
Asp Gln Ala Ser Asp Asp Gly Asp Lys Gly Ser Asp Val Glu Ser Tyr
1345             1350             1355             1360
Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser
            1365             1370             1375
Asp Gly Ser Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val
            1380             1385             1390
Cys Cys
```

```
<210> 4
<211> 4182
<212> DNA
<213> Artificial Sequence

<220>
<223> modified NS3-5A

<221> variation
<222> (2711)...(2711)
<223> n = T or C

<221> variation
<222> (3645)...(3645)
<223> n = A or G

<400> 4
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acacaatcct tcctggcgac ctgcgtcaac ggcgtgtgtt ggaccgttta ccatggtgct 180
ggctcaaaga ccttagccgg cccaaagggg ccaatcaccc agatgtacac taatgtggac 240
caggacctcg tcggctggca ggcgccccc ggggcgcgtt ccttgacacc atgcacctgt 300
ggcagctcag acctttactt ggtcacgaga catgctgacg tcattccggt cgccggcgg 360
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acccggggggg ttgcgaaggc ggtggacttt gtgcccgtag agtccatgga aactactatg 540
cggtctccgg tcttcacgga caactcatcc ccccggccg taccgcagac atttcaagtg 600
gcccacctac acgctcccac tggcagcggc aagagtacta aagtgccggc tgcatatgca 660
gcccaagggt acaaggtgct cgtcctcaat ccgtccgttg ccgctacctt agggtttggg 720
gcgtatatgt ctaaggcaca cggtattgac cccaacatca gaactggggt aaggaccatt 780
accacaggcg cccccgtcac atactctacc tatggcaagt ttcttgccga tggtggttgc 840
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```

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```
aagctgtcag  gcctcggaat  caacgctgtg  gcgtattacc  gggggctcga  tgtgtccgtc  1200
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ggcgactttg  actcagtgat  cgactgtaac  acatgtgtca  cccagacagt  cgacttcagc  1320
ttggatccca  ccttcaccat  tgagacgacg  accgtgcctc  aagacgcagt  gtcgcgctcg  1380
cagcggcggg  gtaggactgg  cagaggtagg  atgggcatct  acaggtttgt  gactccggga  1440
gaacggccct  cgggcatgtt  cgattcctcg  gtcctgtgtg  agtgctatga  cgcgggctgt  1500
gcttggtacg  agctcacccc  cgccgagacc  tcggttaggt  tgcgggccta  cctgaacaca  1560
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gtccttgcag  ctctggccgc  gtattgcctg  acaacaggca  gtgtggtcat  tgtgggtagg  1980
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gagcaattca  agcagaaagc  gctcgggtta  ctgcaaacag  ccaccaaaca  agcggaggct  2160
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caaaccacct  gcccatgtgg  agcacagatc  accggacatg  tcaaaaacgg  ttccatgagg  3060
atcgtcgggc  ctaagacctg  cagcaacacg  tggcatggaa  cattccccat  caacgcatac  3120
accacgggcc  cctgcacacc  ctctccagcg  ccaaactatt  ctagggcgct  gtggcgggtg  3180
gccgctgagg  agtacgtgga  ggtcacgcgg  gtgggggatt  tccactacgt  gacgggcatg  3240
accactgaca  acgtaaagtg  cccatgccag  gttccggctc  ctgaattctt  cacggaggtg  3300
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acattccagg  tcgggctcaa  ccaatacctg  gttgggtcac  agctaccatg  cgagcccgaa  3420
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Gln Asp Ile Gln Pro Ala Ile Gln Ser Ser Trp Pro Lys Leu Glu Gln
        35   40   45
Phe Trp Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu
    50   55   60
Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Val Ala Ser Met Met
65   70   75   80
Ala Phe Ser Ala Ala Leu Thr Ser Pro Leu Pro Thr Ser Thr Thr Ile
                85   90   95

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Ala Gly Ala Thr Gly Phe Val Val Ser Gly Leu Val Gly Ala Ala Val
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Gly Ser Ile Gly Leu Gly Lys Ile Leu Val Asp Val Leu Ala Gly Tyr
    130                 135                 140
Gly Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly
145                 150                 155                 160
Glu Lys Pro Thr Val Glu Asp Val Val Asn Leu Leu Pro Ala Ile Leu
            165                 170                 175
Ser Pro Gly Ala Leu Val Val Gly Val Ile Cys Ala Ala Ile Leu Arg
        180                 185                 190
Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu
        195                 200                 205
Ile Ala Phe Ala Ser Arg Gly Asn His Ala Ser Pro Thr His Tyr Val
    210                 215                 220
Pro Glu Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu
225                 230                 235                 240
Thr Ile Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp
            245                 250                 255
Cys Ser Thr Pro Cys
            260
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